



COPY

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SEQUENCE LISTING

<110> Keating, Mark T.
Splawski, Igor

<120> MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
SYNDROME GENE

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<150> US 09/735,995

<151> 2000-12-14

<150> US 09/226,012

<151> 1999-01-06

<150> US 09/122,847

<151> 1998-07-27

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<170> PatentIn Ver. 2.0

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BEST AVAILABLE COPY

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 Met Pro Val Arg Arg Gly His Val Ala Pro Gln Asn Thr Phe
 1 5 10
 ctg gac acc atc atc cgc aag ttt gag ggc cag agc cgt aag ttc atc 156
 Leu Asp Thr Ile Ile Arg Lys Phe Glu Gly Gln Ser Arg Lys Phe Ile
 15 20 25 30
 atc gcc aac gct cgg gtg gag aac tgc gcc gtc atc tac tgc aac gac 204
 Ile Ala Asn Ala Arg Val Glu Asn Cys Ala Val Ile Tyr Cys Asn Asp

35										40				45						
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gcc	gcg	cag	atc	gcg	cag	gca	ctg	ctg	ggc	gcc	gag	gag	cgc	aaa	gtg	348				
Ala	Ala	Gln	Ile	Ala	Gln	Ala	Leu	Leu	Gly	Ala	Glu	Glu	Arg	Lys	Val					
	80					85					90									
gaa	atc	gcc	ttc	tac	cgg	aaa	gat	ggg	agc	tgc	ttc	cta	tgt	ctg	gtg	396				
Glu	Ile	Ala	Phe	Tyr	Arg	Lys	Asp	Gly	Ser	Cys	Phe	Leu	Cys	Leu	Val					
95					100				105						110					
gat	gtg	gtg	ccc	gtg	aag	aac	gag	gat	ggg	gct	gtc	atc	atg	ttc	atc	444				
Asp	Val	Val	Pro	Val	Lys	Asn	Glu	Asp	Gly	Ala	Val	Ile	Met	Phe	Ile					
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ctc	aat	ttc	gag	gtg	gtg	atg	gag	aag	gac	atg	gtg	ggg	tcc	ccg	gct	492				
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His	Asp	Thr	Asn	His	Arg	Gly	Pro	Pro	Thr	Ser	Trp	Leu	Ala	Pro	Gly					
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cgc	gcc	aag	acc	ttc	cgc	ctg	aag	ctg	ccc	gcg	ctg	ctg	gcg	ctg	acg	588				
Arg	Ala	Lys	Thr	Phe	Arg	Leu	Lys	Leu	Pro	Ala	Leu	Leu	Ala	Leu	Thr					
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gcc	cgg	gag	tcg	tcg	gtg	cgg	tcg	ggc	ggc	gcg	ggc	ggc	gcg	ggc	gcc	636				
Ala	Arg	Glu	Ser	Ser	Val	Arg	Ser	Gly	Gly	Ala	Gly	Gly	Ala	Gly	Ala					
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ccg	ggg	gcc	gtg	gtg	gtg	gac	gtg	gac	ctg	acg	ccc	gcg	gca	ccc	agc	684				
Pro	Gly	Ala	Val	Val	Val	Asp	Val	Asp	Leu	Thr	Pro	Ala	Ala	Pro	Ser					
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agc	gag	tcg	ctg	gcc	ctg	gac	gaa	gtg	aca	gcc	atg	gac	aac	cac	gtg	732				
Ser	Glu	Ser	Leu	Ala	Leu	Asp	Glu	Val	Thr	Ala	Met	Asp	Asn	His	Val					
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Ala	Gly	Leu	Gly	Pro	Ala	Glu	Glu	Arg	Arg	Ala	Leu	Val	Gly	Pro	Gly					
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tct	ccg	ccc	cgc	agc	gcg	ccc	ggc	cag	ctc	cca	tcg	ccc	cgg	gcg	cac	828				
Ser	Pro	Pro	Arg	Ser	Ala															

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acc Thr	tcg Ser 320	gac Asp	tcc Ser	gac Asp	ctc Leu	gtg Val 325	cgc Arg	tac Tyr	cgc Arg	acc Thr	att Ile 330	agc Ser	aag Lys	att Ile	ccc Pro	1068
caa Gln 335	atc Ile	acc Thr	ctc Leu	aac Asn	ttt Phe 340	gtg Val	gac Asp	ctc Leu	aag Lys	ggc Gly 345	gac Asp	ccc Pro	ttc Phe	ttg Leu	gct Ala 350	1116
tcg Ser	ccc Pro	acc Thr	agt Ser	gac Asp 355	cgt Arg	gag Glu	atc Ile	ata Ile	gca Ala 360	cct Pro	aag Lys	ata Ile	aag Lys	gag Glu 365	cga Arg	1164
acc Thr	cac His	aat Asn	gtc Val 370	act Thr	gag Glu	aag Lys	gtc Val 375	acc Thr 375	cag Gln	gtc Val	ctg Leu	tcc Ser 380	ctg Leu	ggc Gly	gcc Ala	1212
gac Asp	gtg Val 385	ctg Leu	cct Pro	gag Glu	tac Tyr	aag Lys	ctg Leu 390	cag Gln	gca Ala	ccg Pro	cgc Arg	atc Ile 395	cac His	cgc Arg	tgg Trp	1260
acc Thr 400	atc Ile	ctg Leu	cat His	tac Tyr	agc Ser	ccc Pro 405	ttc Phe	aag Lys	gcc Ala	gtg Val 410	tgg Trp 410	gac Asp	tgg Trp	ctc Leu	atc Ile	1308
ctg Leu 415	ctg Leu	ctg Leu	gtc Val	atc Ile	tac Tyr 420	acg Thr	gct Ala	gtc Val	ttc Phe	aca Thr 425	ccc Pro	tac Tyr	tcg Ser	gct Ala	gcc Ala 430	1356
ttc Phe	ctg Leu	ctg Leu	aag Lys 435	gag Glu 435	acg Thr	gaa Glu	gaa Glu	ggc Gly 440	ccg Pro	cct Pro	gct Ala	acc Thr	gag Glu	tgt Cys 445	ggc Gly	1404
tac Tyr	gcc Ala	tgc Cys	cag Gln 450	ccg Pro	ctg Leu	gct Ala	gtg Val 455	gtg Val 455	gac Asp	ctc Leu	atc Ile	gtg Val 460	gac Asp	atc Ile	atg Met	1452
ttc Phe	att Ile	gtg Val 465	gac Asp	atc Ile	ctc Leu	atc Ile	aac Asn 470	ttc Phe	cgc Arg	acc Thr	acc Thr	tac Tyr 475	gtc Val	aat Asn	gcc Ala	1500
aac Asn 480	gag Glu	gag Glu	gtg Val	gtc Val	agc Ser	cac His 485	ccc Pro	ggc Gly	cgc Arg	atc Ile	gcc Ala 490	gtc Val	cac His	tac Tyr	ttc Phe	1548
aag Lys 495	ggc Gly	tgg Trp	ttc Phe	ctc Leu	atc Ile 500	gac Asp	atg Met	gtg Val	gcc Ala 505	gcc Ala 505	atc Ile	ccc Pro	ttc Phe	gac Asp	ctg Leu 510	1596
ctc Leu	atc Ile	ttc Phe	ggc Gly 515	tct Ser 515	ggc Gly	tct Ser	gag Glu	gag Glu 520	ctg Leu 520	atc Ile	ggg Gly	ctg Leu	ctg Leu	aag Lys 525	act Thr	1644
gcg Ala	cgg Arg	ctg Leu	ctg Leu 530	cgg Arg	ctg Leu	gtg Val	cgc Arg	gtg Val 535	gcg Ala	cgg Arg	aag Lys	ctg Leu	gat Asp 540	cgc Arg	tac Tyr	1692
tca Ser	gag Glu	tac Tyr	ggc Gly	gcg Ala	gcc Ala	gtg Val	ctg Leu	ttc Phe	ttg Leu	ctc Leu	atg Met	tgc Cys	acc Thr	ttt Phe	gcg Ala	1740

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ctc atc gcg cac tgg cta gcc tgc atc tgg tac gcc atc ggc aac atg Leu Ile Ala His Trp Leu Ala Cys Ile Trp Tyr Ala Ile Gly Asn Met 560 565 570			1788
gag cag cca cac atg gac tca cgc atc ggc tgg ctg cac aac ctg ggc Glu Gln Pro His Met Asp Ser Arg Ile Gly Trp Leu His Asn Leu Gly 575 580 585 590			1836
gac cag ata ggc aaa ccc tac aac agc agc ggc ctg ggc ggc ccc tcc Asp Gln Ile Gly Lys Pro Tyr Asn Ser Ser Gly Leu Gly Gly Pro Ser 595 600 605			1884
atc aag gac aag tat gtg acg gcg ctc tac ttc acc ttc agc agc ctc Ile Lys Asp Lys Tyr Val Thr Ala Leu Tyr Phe Thr Phe Ser Ser Leu 610 615 620			1932
acc agt gtg ggc ttc ggc aac gtc tct ccc aac acc aac tca gag aag Thr Ser Val Gly Phe Gly Asn Val Ser Pro Asn Thr Asn Ser Glu Lys 625 630 635			1980
atc ttc tcc atc tgc gtc atg ctc att ggc tcc ctc atg tat gct agc Ile Phe Ser Ile Cys Val Met Leu Ile Gly Ser Leu Met Tyr Ala Ser 640 645 650			2028
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gcc cgc tac cac aca cag atg ctg cgg gtg cgg gag ttc atc cgc ttc Ala Arg Tyr His Thr Gln Met Leu Arg Val Arg Glu Phe Ile Arg Phe 675 680 685			2124
cac cag atc ccc aat ccc ctg cgc cag cgc ctc gag gag tac ttc cag His Gln Ile Pro Asn Pro Leu Arg Gln Arg Leu Glu Glu Tyr Phe Gln 690 695 700			2172
cac gcc tgg tcc tac acc aac ggc atc gac atg aac gcg gtg ctg aag His Ala Trp Ser Tyr Thr Asn Gly Ile Asp Met Asn Ala Val Leu Lys 705 710 715			2220
ggc ttc cct gag tgc ctg cag gct gac atc tgc ctg cac ctg aac cgc Gly Phe Pro Glu Cys Leu Gln Ala Asp Ile Cys Leu His Leu Asn Arg 720 725 730			2268
tca ctg ctg cag cac tgc aaa ccc ttc cga ggg gcc acc aag ggc tgc Ser Leu Leu Gln His Cys Lys Pro Phe Arg Gly Ala Thr Lys Gly Cys 735 740 745 750			2316
ctt cgg gcc ctg gcc atg aag ttc aag acc aca cat gca ccg cca ggg Leu Arg Ala Leu Ala Met Lys Phe Lys Thr Thr His Ala Pro Pro Gly 755 760 765			2364
gac aca ctg gtg cat gct ggg gac ctg ctc acc gcc ctg tac ttc atc Asp Thr Leu Val His Ala Gly Asp Leu Leu Thr Ala Leu Tyr Phe Ile 770 775 780			2412
tcc cgg ggc tcc atc gag atc ctg cgg ggc gac gtc gtc gtg gcc atc Ser Arg Gly Ser Ile Glu Ile Leu Arg Gly Asp Val Val Val Ala Ile 785 790 795			2460
ctg ggg aag aat gac atc ttt ggg gag cct ctg aac ctg tat gca agg Leu Gly Lys Asn Asp Ile Phe Gly Glu Pro Leu Asn Leu Tyr Ala Arg			2508

800	805	810	
cct ggc aag tcg aac ggg gat gtg cgg gcc ctc acc tac tgt gac cta Pro Gly Lys Ser Asn Gly Asp Val Arg Ala Leu Thr Tyr Cys Asp Leu 815 820 825 830			2556
cac aag atc cat cgg gac gac ctg ctg gag gtg ctg gac atg tac cct His Lys Ile His Arg Asp Asp Leu Leu Glu Val Leu Asp Met Tyr Pro 835 840 845			2604
gag ttc tcc gac cac ttc tgg tcc agc ctg gag atc acc ttc aac ctg Glu Phe Ser Asp His Phe Trp Ser Ser Leu Glu Ile Thr Phe Asn Leu 850 855 860			2652
cga gat acc aac atg atc ccg ggc tcc ccc ggc agt acg gag tta gag Arg Asp Thr Asn Met Ile Pro Gly Ser Pro Gly Ser Thr Glu Leu Glu 865 870 875			2700
ggt ggc ttc agt cgg caa cgc aag cgc aag ttg tcc ttc cgc agg cgc Gly Gly Phe Ser Arg Gln Arg Lys Arg Lys Leu Ser Phe Arg Arg Arg 880 885 890			2748
acg gac aag gac acg gag cag cca ggg gag gtg tcg gcc ttg ggg ccg Thr Asp Lys Asp Thr Glu Gln Pro Gly Glu Val Ser Ala Leu Gly Pro 895 900 905 910			2796
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gat gag ggc cca ggc cgc agc tcc agc ccc ctc cgc ctg gtg ccc ttc Asp Glu Gly Pro Gly Arg Ser Ser Ser Pro Leu Arg Leu Val Pro Phe 945 950 955			2940
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gag gac tgc gag aag agc agc gac act tgc aac ccc ctg tca ggc gcc Glu Asp Cys Glu Lys Ser Ser Asp Thr Cys Asn Pro Leu Ser Gly Ala 975 980 985 990			3036
ttc tca gga gtg tcc aac att ttc agc ttc tgg ggg gac agt cgg ggc Phe Ser Gly Val Ser Asn Ile Phe Ser Phe Trp Gly Asp Ser Arg Gly 995 1000 1005			3084
cgc cag tac cag gag ctc cct cga tgc ccc gcc ccc acc ccc agc ctc Arg Gln Tyr Gln Glu Leu Pro Arg Cys Pro Ala Pro Thr Pro Ser Leu 1010 1015 1020			3132
ctc aac atc ccc ctc tcc agc ccg ggt cgg cgg ccc cgg ggc gac gtg Leu Asn Ile Pro Leu Ser Ser Pro Gly Arg Arg Pro Arg Gly Asp Val 1025 1030 1035			3180
gag agc agg ctg gat gcc ctc cag cgc cag ctc aac agg ctg gag acc Glu Ser Arg Leu Asp Ala Leu Gln Arg Gln Leu Asn Arg Leu Glu Thr 1040 1045 1050			3228
cgg ctg agt gca gac atg gcc act gtc ctg cag ctg cta cag agg cag Arg Leu Ser Ala Asp Met Ala Thr Val Leu Gln Leu Leu Gln Arg Gln			3276

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 Met Thr Leu Val Pro Pro Ala Tyr Ser Ala Val Thr Thr Pro Gly Pro
 1075 1080 1085
 ggc ccc act tcc aca tcc ccg ctg ttg ccc gtc agc ccc ctc ccc acc 3372
 Gly Pro Thr Ser Thr Ser Pro Leu Leu Pro Val Ser Pro Leu Pro Thr
 1090 1095 1100
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 Leu Thr Leu Asp Ser Leu Ser Gln Val Ser Gln Phe Met Ala Cys Glu
 1105 1110 1115
 gag ctg ccc ccg ggg gcc cca gag ctt ccc caa gaa ggc ccc aca cga 3468
 Glu Leu Pro Pro Gly Ala Pro Glu Leu Pro Gln Glu Gly Pro Thr Arg
 1120 1125 1130
 cgc ctc tcc cta ccg ggc cag ctg ggg gcc ctc acc tcc cag ccc ctg 3516
 Arg Leu Ser Leu Pro Gly Gln Leu Gly Ala Leu Thr Ser Gln Pro Leu
 1135 1140 1145 1150
 cac aga cac ggc tcg gac ccg ggc agt tagtggggct gccagtggtg 3563
 His Arg His Gly Ser Asp Pro Gly Ser
 1155
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 <211> 1159
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Cys Glu Leu Cys Gly Tyr Ser Arg Ala Glu Val Met Gln Arg Pro Cys
 50 55 60
 Thr Cys Asp Phe Leu His Gly Pro Arg Thr Gln Arg Arg Ala Ala Ala
 65 70 75 80
 Gln Ile Ala Gln Ala Leu Leu Gly Ala Glu Glu Arg Lys Val Glu Ile
 85 90 95

Ala Phe Tyr Arg Lys Asp Gly Ser Cys Phe Leu Cys Leu Val Asp Val
 100 105 110
 Val Pro Val Lys Asn Glu Asp Gly Ala Val Ile Met Phe Ile Leu Asn
 115 120 125
 Phe Glu Val Val Met Glu Lys Asp Met Val Gly Ser Pro Ala His Asp
 130 135 140
 Thr Asn His Arg Gly Pro Pro Thr Ser Trp Leu Ala Pro Gly Arg Ala
 145 150 155 160
 Lys Thr Phe Arg Leu Lys Leu Pro Ala Leu Leu Ala Leu Thr Ala Arg
 165 170 175
 Glu Ser Ser Val Arg Ser Gly Gly Ala Gly Gly Ala Gly Ala Pro Gly
 180 185 190
 Ala Val Val Val Asp Val Asp Leu Thr Pro Ala Ala Pro Ser Ser Glu
 195 200 205
 Ser Leu Ala Leu Asp Glu Val Thr Ala Met Asp Asn His Val Ala Gly
 210 215 220
 Leu Gly Pro Ala Glu Glu Arg Arg Ala Leu Val Gly Pro Gly Ser Pro
 225 230 235 240
 Pro Arg Ser Ala Pro Gly Gln Leu Pro Ser Pro Arg Ala His Ser Leu
 245 250 255
 Asn Pro Asp Ala Ser Gly Ser Ser Cys Ser Leu Ala Arg Thr Arg Ser
 260 265 270
 Arg Glu Ser Cys Ala Ser Val Arg Arg Ala Ser Ser Ala Asp Asp Ile
 275 280 285
 Glu Ala Met Arg Ala Gly Val Leu Pro Pro Pro Pro Arg His Ala Ser
 290 295 300
 Thr Gly Ala Met His Pro Leu Arg Ser Gly Leu Leu Asn Ser Thr Ser
 305 310 315 320
 Asp Ser Asp Leu Val Arg Tyr Arg Thr Ile Ser Lys Ile Pro Gln Ile
 325 330 335
 Thr Leu Asn Phe Val Asp Leu Lys Gly Asp Pro Phe Leu Ala Ser Pro
 340 345 350
 Thr Ser Asp Arg Glu Ile Ile Ala Pro Lys Ile Lys Glu Arg Thr His
 355 360 365
 Asn Val Thr Glu Lys Val Thr Gln Val Leu Ser Leu Gly Ala Asp Val
 370 375 380
 Leu Pro Glu Tyr Lys Leu Gln Ala Pro Arg Ile His Arg Trp Thr Ile
 385 390 395 400
 Leu His Tyr Ser Pro Phe Lys Ala Val Trp Asp Trp Leu Ile Leu Leu
 405 410 415
 Leu Val Ile Tyr Thr Ala Val Phe Thr Pro Tyr Ser Ala Ala Phe Leu
 420 425 430
 Leu Lys Glu Thr Glu Glu Gly Pro Pro Ala Thr Glu Cys Gly Tyr Ala

435					440					445					
Cys	Gln	Pro	Leu	Ala	Val	Val	Asp	Leu	Ile	Val	Asp	Ile	Met	Phe	Ile
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Val	Asp	Ile	Leu	Ile	Asn	Phe	Arg	Thr	Thr	Tyr	Val	Asn	Ala	Asn	Glu
465					470					475					480
Glu	Val	Val	Ser	His	Pro	Gly	Arg	Ile	Ala	Val	His	Tyr	Phe	Lys	Gly
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Trp	Phe	Leu	Ile	Asp	Met	Val	Ala	Ala	Ile	Pro	Phe	Asp	Leu	Leu	Ile
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Phe	Gly	Ser	Gly	Ser	Glu	Glu	Leu	Ile	Gly	Leu	Leu	Lys	Thr	Ala	Arg
		515					520					525			
Leu	Leu	Arg	Leu	Val	Arg	Val	Ala	Arg	Lys	Leu	Asp	Arg	Tyr	Ser	Glu
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Tyr	Gly	Ala	Ala	Val	Leu	Phe	Leu	Leu	Met	Cys	Thr	Phe	Ala	Leu	Ile
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Ala	His	Trp	Leu	Ala	Cys	Ile	Trp	Tyr	Ala	Ile	Gly	Asn	Met	Glu	Gln
			565						570					575	
Pro	His	Met	Asp	Ser	Arg	Ile	Gly	Trp	Leu	His	Asn	Leu	Gly	Asp	Gln
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Ile	Gly	Lys	Pro	Tyr	Asn	Ser	Ser	Gly	Leu	Gly	Gly	Pro	Ser	Ile	Lys
		595					600					605			
Asp	Lys	Tyr	Val	Thr	Ala	Leu	Tyr	Phe	Thr	Phe	Ser	Ser	Leu	Thr	Ser
	610					615					620				
Val	Gly	Phe	Gly	Asn	Val	Ser	Pro	Asn	Thr	Asn	Ser	Glu	Lys	Ile	Phe
625					630					635					640
Ser	Ile	Cys	Val	Met	Leu	Ile	Gly	Ser	Leu	Met	Tyr	Ala	Ser	Ile	Phe
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Gly	Asn	Val	Ser	Ala	Ile	Ile	Gln	Arg	Leu	Tyr	Ser	Gly	Thr	Ala	Arg
			660					665					670		
Tyr	His	Thr	Gln	Met	Leu	Arg	Val	Arg	Glu	Phe	Ile	Arg	Phe	His	Gln
		675					680					685			
Ile	Pro	Asn	Pro	Leu	Arg	Gln	Arg	Leu	Glu	Glu	Tyr	Phe	Gln	His	Ala
	690					695					700				
Trp	Ser	Tyr	Thr	Asn	Gly	Ile	Asp	Met	Asn	Ala	Val	Leu	Lys	Gly	Phe
705					710					715					720
Pro	Glu	Cys	Leu	Gln	Ala	Asp	Ile	Cys	Leu	His	Leu	Asn	Arg	Ser	Leu
			725						730					735	
Leu	Gln	His	Cys	Lys	Pro	Phe	Arg	Gly	Ala	Thr	Lys	Gly	Cys	Leu	Arg
			740					745					750		
Ala	Leu	Ala	Met	Lys	Phe	Lys	Thr	Thr	His	Ala	Pro	Pro	Gly	Asp	Thr
		755					760					765			
Leu	Val	His	Ala	Gly	Asp	Leu	Leu	Thr	Ala	Leu	Tyr	Phe	Ile	Ser	Arg
	770					775					780				

Gly Ser Ile Glu Ile Leu Arg Gly Asp Val Val Val Ala Ile Leu Gly
 785 790 795 800
 Lys Asn Asp Ile Phe Gly Glu Pro Leu Asn Leu Tyr Ala Arg Pro Gly
 805 810 815
 Lys Ser Asn Gly Asp Val Arg Ala Leu Thr Tyr Cys Asp Leu His Lys
 820 825 830
 Ile His Arg Asp Asp Leu Leu Glu Val Leu Asp Met Tyr Pro Glu Phe
 835 840 845
 Ser Asp His Phe Trp Ser Ser Leu Glu Ile Thr Phe Asn Leu Arg Asp
 850 855 860
 Thr Asn Met Ile Pro Gly Ser Pro Gly Ser Thr Glu Leu Glu Gly Gly
 865 870 875 880
 Phe Ser Arg Gln Arg Lys Arg Lys Leu Ser Phe Arg Arg Arg Thr Asp
 885 890 895
 Lys Asp Thr Glu Gln Pro Gly Glu Val Ser Ala Leu Gly Pro Gly Arg
 900 905 910
 Ala Gly Ala Gly Pro Ser Ser Arg Gly Arg Pro Gly Gly Pro Trp Gly
 915 920 925
 Glu Ser Pro Ser Ser Gly Pro Ser Ser Pro Glu Ser Ser Glu Asp Glu
 930 935 940
 Gly Pro Gly Arg Ser Ser Ser Pro Leu Arg Leu Val Pro Phe Ser Ser
 945 950 955 960
 Pro Arg Pro Pro Gly Glu Pro Pro Gly Gly Glu Pro Leu Met Glu Asp
 965 970 975
 Cys Glu Lys Ser Ser Asp Thr Cys Asn Pro Leu Ser Gly Ala Phe Ser
 980 985 990
 Gly Val Ser Asn Ile Phe Ser Phe Trp Gly Asp Ser Arg Gly Arg Gln
 995 1000 1005
 Tyr Gln Glu Leu Pro Arg Cys Pro Ala Pro Thr Pro Ser Leu Leu Asn
 1010 1015 1020
 Ile Pro Leu Ser Ser Pro Gly Arg Arg Pro Arg Gly Asp Val Glu Ser
 1025 1030 1035 1040
 Arg Leu Asp Ala Leu Gln Arg Gln Leu Asn Arg Leu Glu Thr Arg Leu
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 Ser Ala Asp Met Ala Thr Val Leu Gln Leu Leu Gln Arg Gln Met Thr
 1060 1065 1070
 Leu Val Pro Pro Ala Tyr Ser Ala Val Thr Thr Pro Gly Pro Gly Pro
 1075 1080 1085
 Thr Ser Thr Ser Pro Leu Leu Pro Val Ser Pro Leu Pro Thr Leu Thr
 1090 1095 1100
 Leu Asp Ser Leu Ser Gln Val Ser Gln Phe Met Ala Cys Glu Glu Leu
 1105 1110 1115 1120
 Pro Pro Gly Ala Pro Glu Leu Pro Gln Glu Gly Pro Thr Arg Arg Leu

1125 1130 1135
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1140 1145 1150

His Gly Ser Asp Pro Gly Ser
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<211> 63
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:Hypothetical
sequence for the example of calculating homology.

[illegible]

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<210> 6
<211> 130
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:Hypothetical
sequence for example of calculating homology.

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gattgactag                                     130
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<210> 7
<211> 20
<212> DNA
<213> Homo sapiens
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<210> 8
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